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## Patent claims

- A homoserine transsuccinylase which, as compared 1. homoserine transsuccinylase wild-type 5 exhibits a reduced sensitivity L-methionine or SAM, with the wild-type enzyme possessing an amino acid sequence which comprises a constituent sequence TyrGlnXaaThrPro, with the Thr of this constituent sequence being between 10 position 285 and 310 of the amino acid sequence and with position 1 being the starting methionine, characterized in that it exhibits a change of at least 2 amino acids as compared with the wild-type enzyme, with this change being in the Thr of the 15 constituent sequence or C-terminally thereof.
  - 2. A homoserine transsuccinylase as claimed in claim 1, characterized in that it exhibits a change of at least 5 amino acids, preferably of at least 10 amino acids.
- 3. transsuccinylase homoserine claimed as claim 1 or 2, characterized in that it exhibits a resistance toward the inhibitors SAM and/or 25 L-methionine which is increased (increased Ki) at 2-fold as' compared with that the wild-type enzyme.
- 4. A homoserine transsuccinylase as claimed in one of claims 1 to 3, characterized in that it contains one of the mutations listed in Table 1.
  - 5. A metA allele which encodes a homoserine transsuccinylase as claimed in one of claims 1 to 4.
  - 6. A plasmid, characterized in that it contains a metA allele as claimed in claim 5 together with a promoter.

7. A microorganism strain, characterized in that it contains a feedback-resistant metA allele as claimed in claim 5.

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- 8. A microorganism strain as claimed in claim 7, characterized in that it is a Gram-negative bacterial strain, preferably E. coli.
- 10 9. A method for preparing L-methionine or SAM by culturing a microorganism strain as claimed in claim 7 or 8.